In the claims:

Please amend the claims as follows.

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1. (Currently amended) A cell composition comprising a population of non-yeast eukaryotic cells [containing] transfected with a diverse population of about 10 or more variant nucleic acids, wherein each cell expresses a single variant nucleic acid of said population of variant nucleic acids [being expressed in a different cell] and wherein said variant nucleic acid is located within each cell at an identical site in the genome.

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2. (Currently amended) The cell composition of claim 1, wherein said variant nucleic acids encode polypeptides having [have] predetermined amino acid changes at preselected positions [within] relative to a parent amino acid sequence.

3. (Original) The cell composition of claim 1, wherein said variant nucleic acids are integrated in each cell by a site specific recombination sequence.

4. (Original) The cell composition of claim 1, wherein said cells express Cre recombinase or Flp recombinase.

5. (Original) The cell composition of claim 1, wherein said site in the genome comprises two lox sites.

6. (Original) The cell composition of claim 5, wherein at least one of said lox sites is a loxP site.

7. (Original) The cell composition of claim 5, wherein at least one of said lox sites is a lox511 site.

8. (Original) The cell composition of claim 5, wherein said site in the genome comprises two non-identical lox sites.

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9. (Original) The cell composition of claim 8, wherein said site in the genome comprises a loxP site and a lox511 site.

10. (Original) The cell composition of claim 1, wherein said cell is a mammalian cell.

11. (Withdrawn) A method of identifying a polypeptide exhibiting optimized activity, comprising:

(a) screening the cell composition of claim 1 for an activity associated with a parent polypeptide of a diverse population of variant polypeptides encoded by said variant nucleic acids; and

(b) identifying a variant polypeptide exhibiting an optimized activity relative to said parent polypeptide.

12. (Withdrawn) A method of identifying a binding ligand, comprising:

(a) contacting the cell composition of claim 1 with one or more ligands; and

(b) identifying a ligand that binds to one of said variant nucleic acids.

A9 Cont.

13. (Withdrawn) A method of identifying a binding ligand, comprising:

(a) contacting the cell composition of claim 1 with one or more ligands, said cells containing a diverse population of variant polypeptides encoded by said variant nucleic acids; and

(b) identifying a ligand that binds to a polypeptide encoded by said variant nucleic acids.

14. (Original) A cell composition comprising a population of non-yeast eukaryotic cells containing a population of 10 or more variant nucleic acids, each of said variant nucleic acids being expressed in a different

cell and integrated in the genome of each cell by a site specific recombination sequence.

15. (Amended) The cell composition of claim 14, wherein said variant nucleic acids encode polypeptides having [have] predetermined amino acid changes at preselected positions [within] relative to a parent amino acid sequence.

16. (Original) The cell composition of claim 14, wherein said cells express Cre recombinase or Flp recombinase.

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cont.

17. (Original) The cell composition of claim 14, wherein said site in the genome comprises two lox sites.

18. (Original) The cell composition of claim 17, wherein at least one of said lox sites is a loxP site.

19. (Original) The cell composition of claim 17, wherein at least one of said lox sites is a lox511 site.

20. (Original) The cell composition of claim 17, wherein said site in the genome comprises two non-identical lox sites.

21. (Original) The cell composition of claim 20, wherein said site in the genome comprises a loxP site and a lox511 site.

22. (Original) The cell composition of claim 14, wherein said variant nucleic acids are integrated at a single site in the genome of each cell.

23. (Original) The cell composition of claim 14, wherein each of said variant nucleic acids is expressed in a different cell.

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24. (Original) The cell composition of claim 14, wherein said cell is a mammalian cell.

25. (Withdrawn) A method of identifying a polypeptide exhibiting optimized activity, comprising:

(a) screening the cell composition of claim 14 for an activity associated with a parent polypeptide of a diverse population of variant polypeptides encoded by said variant nucleic acids; and

(b) identifying a variant polypeptide exhibiting an optimized activity relative to said parent polypeptide.

26. (Withdrawn) A method of identifying a binding ligand, comprising:

(a) contacting the cell composition of claim 14 with one or more ligands; and

(b) identifying a ligand that binds to one of said variant nucleic acids.

27. (Withdrawn) A method of identifying a binding ligand, comprising:

(a) contacting the cell composition of claim 14 with one or more ligands, said cells containing a diverse population of variant polypeptides encoded by said variant nucleic acids; and

A2 Cont.

(b) identifying a ligand that binds to a polypeptide encoded by said variant nucleic acids.

28. (Withdrawn) A cell composition comprising a population of non-yeast eukaryotic cells containing a diverse population of 10 or more heterologous nucleic acid fragments, said heterologous nucleic acid fragments comprising distinct species of nucleic acid fragments, each of said heterologous nucleic acid fragments being expressed in a different cell and located within each cell at an identical site in the genome.

29. (Withdrawn) The cell composition of claim 28, wherein said heterologous nucleic acid fragments are integrated in each cell by a site specific recombination sequence.

30. (Withdrawn) The cell composition of claim 28, wherein said cells express Cre recombinase or Flp recombinase.

31. (Withdrawn) The cell composition of claim 28, wherein said site in the genome comprises two lox sites.

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32. (Withdrawn) The cell composition of claim 31, wherein at least one of said lox sites is a loxP site.

33. (Withdrawn) The cell composition of claim 31, wherein at least one of said lox sites is a lox511 site.

34. (Withdrawn) The cell composition of claim 31, wherein said site in the genome comprises two non-identical lox sites.

35. (Withdrawn) The cell composition of claim 34, wherein said site in the genome comprises a loxP site and a lox511 site.

36. (Withdrawn) The cell composition of claim 28, wherein said cell is a mammalian cell.

37. (Withdrawn) A method of identifying a binding ligand, comprising:

(a) contacting the cell composition of claim 28 with one or more ligands; and

(b) identifying a ligand that binds to one of said heterologous nucleic acid fragments.

A2 cont.

38. (Withdrawn) A method of identifying a binding ligand, comprising:

(a) contacting the cell composition of claim 28 with one or more ligands, said cells containing a diverse population of polypeptides encoded by said heterologous nucleic acid fragments; and

(b) identifying a ligand that binds to a polypeptide encoded by said heterologous nucleic acid fragments.

39. (Withdrawn) A method of identifying a polypeptide receptor for a ligand, comprising:

(a) contacting a population of non-yeast eukaryotic cells containing a diverse population of 10 or more heterologous nucleic acid fragments encoding

polypeptides with a ligand, said heterologous nucleic acid fragments comprising distinct species of nucleic acid fragments, each of said heterologous nucleic acid fragments being expressed in a different cell and located within each cell at an identical site in the genome; and

(b) identifying a polypeptide encoded by said heterologous nucleic acid fragments that binds to said ligand.

A9 cont.

40. (Withdrawn) A method of identifying a functional polypeptide fragment, comprising:

(a) introducing a diverse population of 10 or more heterologous nucleic acid fragments into a non-yeast eukaryotic cell to generate a population of cells, said heterologous nucleic acid fragments comprising distinct species of nucleic acid fragments, each of said nucleic acid fragments being expressed in a different cell and located within each cell at an identical site in the genome;

(b) screening said population of cells for a functional activity; and

(c) identifying a polypeptide encoded by said nucleic acid fragments having said functional activity.

41. (New) A method for generating the cell composition of claim 1, comprising transfecting a population of non-yeast eukaryotic cells with a diverse population of about 10 or more variant nucleic acids, whereby each of said variant nucleic acids integrates at an identical site in the genome and each cell expresses a single variant nucleic acid of said population of variant nucleic acids.

A9 cont.

42. (New) A method for generating the cell composition of claim 14, comprising transfecting a population of non-yeast eukaryotic cells with a diverse population of about 10 or more variant nucleic acids, whereby each of said variant nucleic acids integrates at an identical site in the genome and each cell expresses a single variant nucleic acid of said population of variant nucleic acids.

43. (New) A method for generating the cell composition of claim 28, comprising transfecting a population of non-yeast eukaryotic cells with a diverse population of about 10 or more heterologous nucleic acid fragments, whereby each of said heterologous nucleic acid fragments integrates at an identical site in the genome and each cell expresses a single heterologous nucleic acid fragment of said population of heterologous nucleic acid fragments.